```
31/11
1/1
age geg get eeg ete teg get ggg gtt egt eac tyg geg egg gat ttg gee geg ggg
     à PLSAG V ROHWOARDLAAAG
G A
                               91/31
ctc ogg age ege teg etc eeg aca egg etc aeg atg ege gge gae agg gee ggg gge
LRSRSLPTRLTMRGD
                                             R
                               151/51
121/41
ccc gtg ctc cag ttc act aac tgc cgg atc ctg cgc gga ggg aaa ctg ctc agg gag gat
P V L Q F T N C R I L R G G K L
                                                L R E D
                               211/71
181/61
ctg tgg gtg cgc gga ggc cgc atc ttg gac ccz gag aag ctg ttc ttt gag gag cgc
                              PEKLFF
                                                EERR
      V R G G R I L D
L W
                               271/91
241/81
gtg gee gae gag egg egg gae tge ggg gge ege ate ttg get eee gga tte ate gae gtg
V A D E R R D C G G R I L A
                                          P G
                               331/111
301/101
cag atc aac cgt gga TTT GGT GTT GAC TTC TCT CAA GCC ACG GAG GAC GTG GGT TCG GGG
                       D F S Q A T E
                                             D
QINRGFGV
                               391/131
GTT GCC CTC GTG GCC CGG AGG ATC CTG TCG CAC GGC GTC ACC TCC TTC TGC CCC ACC CTG
                        L S H G V
                                       Т
                                          S
                                             F
         V A R R
V A L
                     I
                               451/151
421/141
GTC ACT TCC CCA CCG GAG GCT TAT CAC AAG GTT GTT CCT CAG ATC CCT GTG AAG AGT GGT
V T S P P E A Y H K V V P Q I P V K S
                               511/171
GGT CCC CAT GGG GCA GGG GTC CTC GGG CTG CAC CTG GAG GGC CCC TTC ATC AGC CGG GAG
G P H G A G V L G L H L E G P F
                              571/191
541/181
AAG CGG GGC GCG CAC CCC GAG GCC CAC CTC CGC TCC TTC GAG GCC GAT GCC TTC CAG GAC
                                          ADAFQD
                       HLRSFE
K R G A H P E A
                              631/211
601/201
TTG CTG GCC ACC TAC GGG CCC CTG GAC AAT GTC CGC ATC GTG ACG CTG GCC CCA GAG TTG
                                       V T L A
                              V R
LLATYGPL
                        D N
                              691/231
661/221
GGC CGT AGC CAC GAA GTG ATC CGG GCG CTG ACG GCC CGT GGC ATC TGC GTG TCC CTA GGG
                              TARGI
                                                V
GRSHEV
                     R
                          L
                  I
                       A
                              751/251
721/241
CAC TCA GTG GCT GAC CTG CGG GCG GCA GAG GAT GCT GTG TGG AGC GGA GCC ACC TTC ATC
                          EDAVWSGAT
H S V A D L R A A
                              811/271
781/261
ACC CAC CTC TTC AAC GCC ATG CTG CCT TTC CAC CGC GAC CCA GGC ATC GTG GGG CTC
  H L F N A M L P F H H R D P G
```

```
871/291
 CTG ACC AGC GAC CGG CTG CCC GCA GGC CGC TGC ATC TTC TAT GGG ATG ATT GCA GAT GGC
 L T S D R L P A G R C I F Y G M I A D
                                931/311
 901/301
 ACG CAC ACC AAC CCC GCC GCC CTG CGG ATC GCC CAC CGT GCC CAT CCC CAG GGG CTG GTG
 THINPAALRIAHRAHPQGLV
                                991/331
 961/321
CTG GTC ACC GAT GCC ATC CCT GCC. TTG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG
         DA. IPALGLGNGRHTL
L V T
                                1051/351
1021/341
CAG GAA GTG GAA GTG GAC GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG
O E V E V D G L T A Y V A G E R P
                                1111/371
1081/361
GGT CCC AGG TCC CAG CCC GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA GCC TGC CCT CTC
                              A H D P P R A
G P R S Q P A C Q
                           V
                                1171/391
1141/381 .
TGC TCT CAA GGC ACC AAG ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG
C S Q G T K T L S G S I A P M N V C V R
7201/401
                               1231/411
CAC TTC CTG CAG GCC ACA GGC TGC AGC ATG GAG TCG GCC CTG GAG GCT GCA TCC CTG CAC
        QATGCSMESALEAASLH
1251/421
                               1291/431
CCC GCC CAG TTG CTG GGG CTG GAG AAG AGT AAG GGG ACC CTG GAC TTT GGT GCT GAC GCA
PAQ
        LLGLEKSKGT
                                       L D F
1321/441
                               1351/451
GAC TTC GTG GTG CTC GAC GAC TCC CTT CAC GTC CAG GCC ACC TAC ATC TCG GGT GAG CTG
D F V V L D D S L H
                               V Q A
                                       TYISGEL
1381/461
                               1411
GTG TGG CAG GCG GAC GCA GCT AGG CAG TGA CAA GGA CCT CGG CTG AGA GGA CAC CTG GCC
VWQADAA
                    R
1441
                               1471.
GCA GCG GGA TGC CAT CAG GGC CGG GTG GTT GGG GAG CTG GTC TCC AGG GAG TGA GTC GGG
1501
```

AGC CCT GCT GGA T

cloned deduced	1	MFARSAGLCFPWYPGYSHGGDAEEYLAQHPTPT
cloned deduced	1 34	GRGAERRPRPPDSSAEGDPGMLKPCGCYPSPQK
cloned deduced	1 67	YALKYGAPFCTCGCFQRFHLPKACPGQQGSPES
cioned deduced	100	ARPRNROPYATONGPAPRPOYLPGSSSRCCHGY
cloned deduced	1 133	I C F L F D S S O T A E Y E Y G W G G D T G S O L R P L L R G A Y
cloned deduced	1 166	YHSRMWDSQKEDSKPDILRLQNTQLFHSYSLST
cloned deduced	1 199	DGTOYSPGAHYCSPTGAGCPRPCADTPGPQPQP
cloned deduced	1 232	MDLRYGQRPPYEPPPEPTLLALQRPQRLHHHLF
cloned deduced	1 255	LAGLQQQRSYEPMRYKMELPACGATLSLYPSLP
cloned deduced	1 298	AFSIPRHQSQSSTPCPFLGCRPCPQLSMDTPMP

cloned deduced	1 331	E	- L	ā	Ý	G	- P	Q	Ē	- Q	E	L	R	- Q	L	L	- Н	- K	D	ĸ	s	- К	R	S	- K	E	Ÿ	Ā	T	P	Å	- Q	P	S
cloned deduced	1 . 364	P	T	s	ā	Y	- P	- Д	A	Д	C	Ţ	- A	c	Ā	Ÿ	Ā	s	- S	Ÿ	Ÿ	ĸ	ā	- K	- L	- Å	Ē	Ý	-	Ĺ	К	- K	ā	- Q
cloned deduced	1 397	- À	ء غر	L	Ē	A	- T	Ÿ	Н	p	7	s	<u>-</u> Р	G	-	P	- Y	R	S	Q	G	P	c	s S	- G :	- Q	C	Þ	Ċ	s	Ÿ	P	T	P
cloned deduced	1 -430	- L	К	ā	Р	W	- Н	<u>.</u> S	F	C	- R	- T	L	Ē	P	L	E	T	Ē	G	- اخ	- T	A	- S 1	- M	L	S	s	F	L	P	- P	Ÿ	- P
cloned deduced	1 463	S	L	0	S	- D	- P	- P	E	Н	F	P	L	R	K	- T	Ÿ	S	E	- P	7	L	K	L	- R	- Y	K	P	- K	- K	S	L	E	R
cloned deduced	1 496	R	K	7	P	- L	L	- R	K	E	s S	- Д	P	P	S	L	- R	R	R	- P	Å	Е	- T	- L (۔ ا 3	D	s	· S	- Р	S	S	S	· S	- T
cloned deduced	1 529	P	- Д	S	G	C	- S	- S	p	N	D	S	- E	- Н	G	- p	7	p	-	ī.	Ğ	S	- E .	- Д 1	_	_ L 1	G	- O	- R	L	R	L	- Q	Ē
cloned deduced	1 562	Ť	S	- Y	_ <u>A</u>	Р	- F	- A	Ŀ	P	· T	Ÿ	s	L	- L	P	- Д	-	T	Ī	- G	- L	- Р.	- A	- ⊃ ,	<u>-</u>	R	- Å	- D	S	D	- R	- R	- T
cioned deduced	1 595	- Н	- Р	- T	L	G	P	- R	Э	P	-	L	G	S	Р	- Н	- T	P	L	F	L	P	<u>.</u> Н (G I	-	Ē	P	Ė	- Å	G	G	- T	- L	- P
cloned deduced	1 628		R	- L (Q	P	1	L	- L	L	D	Р	S	G	s	- Н	- A	P	L	- L	- T	Y	P(3 l	- (<u>.</u>	P	L	. Р	F	Н	- F.	_ A (a

Fig. 7 (b)

cloned deduced	661	SLMTTERLSGSGLHWPLSRTRSEPLPPSATAF	P
cloned deduced	694	P P G P M Q P R L E O L K T H V O V I K R S A K P S E K P R L R	
cloned	25	I PS A ED L ET DGGG PGQ Y Y DDG L EHRELGHGO P	;
deduced	. 727	I PS A ED L ET DGGG PGO Y Y DDG L EHRELGHGO P	
cloned	58	A RG P A P L O O H P O Y L L W E O O R L A G R L P R G S T G D	1
deduced	760	A RG P A P L O O H P O Y L L W E O O R L A G R L P R G S T G D	
cloned deduced	91 793	Y L L P L A Q G G H R P L S R A Q S S P A A P A S L S A P E P A Y L L P L A Q G G H R P L S R A Q S S P A A P A S L S A P E P A	
cloned	124	O A R Y L S S S E T P A R T L P F T T G L I Y D S Y M L K H Q C	- 1
deduced	826	Q A R Y L S S S E T P A R T L P F T T G L I Y D S Y M L K H Q C	
cloned	157	CGDNSRHPEHAGRIQS I WSRLOERGLRSQCEC	1
deduced	859	CGDNSRHPEHAGRIQS I WSRLOERGLRSQCEC	
cloned	190	RGRKAS LEELQS YHS ERHYLL YGTNPLS RLKLI	
deduced	892	RGRKAS LEELQS YHS ERHYLL YGTNPLS RLKLI	

cloned deduced	223 925	NGKLAGLLAQRMFYMLPCGGYG
cloned deduced	245 958	LAPTYPQGLSRYSWGLKPPPGPNPKSRPAPCPW
cloned deduced	245 991	GPGRGYGTTPLGPGSCYKPWMMRALTLAPQVDT
cloned	248	DT I WHELHS SHAARWAAGS YTD LAFKYAS RELK
deduced	1024	DT I WHELHS SHAARWAAGS YTD LAFKYAS RELK
cloned	281	NG FAYYR PPGHHADHS TAMG F C F F NS YA I A C RQ
deduced	1057	NG F A Y Y R P P G H H A D H S T A MG F C F F N S Y A I A C RQ
cloned	314	LQQQSKASKILIYDWDYHHGNGTQQTFYQDPSY
deduced	1090	LQQQSKASKILIYDWDYHHGNGTQQTFYQDPSY
cioned	347	LY I S L H R H D D G N F F P G S G A Y D E Y G A G S G E G F N Y
deduced	1123	LY I S L H R H D D G N F F P G S G A Y D E Y G A G S G E G F N Y
cioned	380	NYAWAGGLDPPMGDPEYLAAFRIYYMPIAREFS
deduced	1156	NYAWAGGLDPPMGDPEYLAAFRIYYMPIAREFS

	*	and the control of th	
cloned	41⊃	PDLYLYSAGFDAAEGHPAPLGGYHYSAKCFGY	
. deduced	1189	PDLYLYSAGFDAAEGHPAPLGGYHYSAKCFGY	
cloned	446	TQQLMNLAGGAYYLALEGGHDLTAICDASEAC	
deduced	1222	TQQLMNLAGGAYYLALEGGHDLTAICDASEAC	
cloned	479	AALLGNRYDPLSEEGWKOKPNLNSIRSLEAVI	R
deduced	1255	AALLGNRYDPLSEEGWKOKPN®NAIRSLEAVI	R
cloned	512	YHS	-
deduced	1288		C
cloned	515	Q P G D L L V W S K I P Y S D P G S N G E H P P Y R G Y P L S I	-
deduced	1321		P
cloned deduced	515 1354	PDGASRAYQTYAPQGKYWGCMQRLASCPDSWYR	
cloned	533	RYPGADKEEYEAYTALAS LS YGILAEDRPS EO L	- }
deduced	1387	RYPGADKEEYEAYTALAS LS YGILAEDRPS EO L	
cloned	566	Y E E E P M N L	
deduced	1420	Y E E E P M N L	

		PQPQPMDLRVGQRPPVEPPPEPTLLALQRPQRLHHHLFLAGL 2 : : : : : : : : : : : : : :	-
26	59	QQQRSVEPMRVKMELPACGATLSLVPSLPAFSIPRHQSQS 3	08
9			41
14		ELEKQHREQKLQQLKNKEKGKES 16	54
35 16		PAQPSPTSQVPAAACVACAVASSVVKQKLAEVILKKQQAALERTVHPNSP 40 : : : : : : : :	_
40	9 (7
19		: : : : :: NHCISSDPRYWYGKTQHSSLDQS 21	4
		LPPVPSLPSDPPEHFPLRKTVSEPNLKLRYKPK.KSLERR 49 :: :	-
	:	KNPLLRKESAP. PSLRRRPAETLGDSSPSSSTPASGCSSPNDS 539 :: ::: : :: : : : : SSPLLRRKDGPVVTALKKRPLDV TDSACSSAPGSGPSSPNNSSGSVS 31:	
540 312		EHGPNPILGS. EALLGQRLRLQETSVAPFALPTVSLLBAITLGLPA. 584	
585 362		PARADSDRRTHPTLGPRGPILGSPH.TPLFLPHGLEPEAGGTLP 627 :: :: :: : : :: :	
628 412	S:	FRLOPILLLDPSGSHAPLLTVPGLGPLPFHFAQSLMTTERLSGSGL 673 :: : :: : : : :: : PLLQHMVLLEQPPAQAPLVTGLGALPLH.AQSLVGADRVSPSIHKLRQ 458	
674	HV	WPLSRTRSEPLPPSATAPPPPGPMQPRLEQLKTHVQVIKRS 715	
459	HI	: : : : : : : : RPLGRTQSAPLPQNAQALQHLVIQQQHQQFLEKHKQQFQQQQLQMNKII 508	
716	Al	KPSEKPRLRQIPSAEDLETDGGGPG 741	
509	Pk	:: : :::: KPSEPARQPESHPEETEEELREHQALLDEPYLDRLPGQKEAHAQAGV 556	
742	QV	VVDDGLEHRELGHGQPEARGPAPLQQHPQVLLWEQQR 779	
557	QV	:: :	
780	LA.	AGRLPRGSTGDTVLLPLAQGGHRPLSRAQSSPA.APASLSAPEPASQAR 828	
602	ΞH	:: ::: : :: : : :: HQLRNYQASMEAAGIPVSFGGHRPLSRAQSSPASATFPVSVQEPPTKPR 651	
829	VL	LSSSETPARTLPFTTGLIYDSVMLKHQCSCGDNSRHPEHAGRIQSIWSR 878	
652		: :: ::	

879	LQERGLRSQCECLRGRKASLEELQSVHSERHVLLYGTNPLSRLKLDNGKL	928
689		738
929	AGLLAQRMFVMLPCGGVGPLATLSAFLASLAPTVPQGLSRVSWGLKPPPG	978
739	• • • • • • • • • • • • • • • • • • • •	755
979	PNPKSRPAPCPWGPGRGVGTTPLGPGSCVKPWMMRALTLAPQVDTDTIWN	1028
756		763
1029		1078
764		813
1079		
814	YFNSVAVAAKLLQQRLSVSKILIVDWDVHHGNGTQQAFYSDPSVLYMSLH	863
1129		1178 913
		1228
	VVM TACET SEDAVIV SAGT DAGEGREAFLIGGTNV SARCEGIM TO CONTROL OF THE	
1229	AGGAVVLALEGGHDLTAICDASEACVAALLGNRVDPLSEEGWKOKPNLNA	1278
964	: : :: :: :: AGGRIVLALEGGHDLTAICDASEACVSALLGNELDPLPEKVLQQRPNANA	10,13
1279	IRSLEAVIRVHSKCGDGTLAELRLKDLGGTLPHRGQILGFRCQPGDLLLV : : : : :	1328
1014		1025
1329	WSKIPVSDPGSNGEHPPVRGYPLSPPDGASRAYQTVAPQGKYWGCMQRLA 1	378
L026	KYWRCLQRTT 1	.035
379		26
.036	: :: ::: : :	84